RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/236,995D

DATE: 10/29/2001
TIME: 14:44:35

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\10292001\I236995D.raw

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 4 <110> APPLICANT: Mahajan, Pramod
 5         Zuo, Zhuang
 7 <120> TITLE OF INVENTION: Poly ADP-Ribose Polymerase Gene and its
 8         Uses
10 <130> FILE REFERENCE: 5718-34
12 <140> CURRENT APPLICATION NUMBER: US 09/236,995D
13 <141> CURRENT FILING DATE: 1999-01-26
15 <150> PRIOR APPLICATION NUMBER: US 60/072,785
16 <151> PRIOR FILING DATE: 1998-01-27
18 <160> NUMBER OF SEQ ID NOS: 5
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 2949
24 <212> TYPE: DNA
25 <213> ORGANISM: Zea mays
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)...(2949)
31 <221> NAME/KEY: misc_feature
32 <222> LOCATION: 1584, 1588, 2078, 2107
33 <223> OTHER INFORMATION: n = A,T,C or G
35 <400> SEQUENCE: 1
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37 Met Ala Ala Pro Pro Lys Ala Trp Lys Ala Glu Tyr Ala Lys Ser Gly
38 1               5                   10                  15
40 cgg gcc tcg tgc aag tca tgc cgg tcc cct atc gcc aag gac cag ctc    96
41 Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Gln Leu
42              20                  25                  30
44 cgt ctt ggc aag atg gtt cag gcg tca cag ttc gac ggc ttc atg ccg   144
45 Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro
46          35                  40                  45
48 atg tgg aac cat gcc agg tgc atc ttc agc aag aag aac cag ata aaa   192
49 Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys
50      50                  55                  60
52 tcc gtt gac gat gtt gaa ggg ata gat gca ctt aga tgg gat gat caa   240
53 Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln
54 65                  70                  75                  80
56 gag aag ata cga aac tac gtt ggg agt gcc tca gct ggt aca agt tct   288
57 Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly Thr Ser Ser
58                  85                  90                  95
60 aca gct gct cct cct gag aaa tgt aca att gag att gct cca tct gcc   336
61 Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala
62              100                 105                 110
64 cgt act tca tgt aga cga tgc agt gaa aag att aca aaa gga tcg gtc   384
65 Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys Gly Ser Val
66          115                 120                 125
68 cgt ctt tca gct aag ctt gag agt gaa ggt ccc aag ggt ata cca tgg   432
```

DNA Sequence; it is not necessary that unknown PRTs in coded regions are listed. MH

ENTERED
P.5

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 69 Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly Ile Pro Trp
 70         130                 135                 140
 72 tat cat gcc aac tgt ttc ttt gag gta tcc ccg tct gca act gtt gag   480
 73 Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu
 74 145                 150                 155                 160
 76 aag ttc tca ggc tgg gat act ttg tcc gat gag gat aag aga acc atg   528
 77 Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met
 78                 165                 170                 175
 80 ctc gat ctt gtt aaa aaa gat gtt ggc aac aat gaa caa aat aag ggt   576
 81 Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn Glu Gln Asn Lys Gly
 82                 180                 185                 190
 84 tcc aag cgc aag aaa agt gaa aat gat att gat agc tac aaa tcc gcc   624
 85 Ser Lys Arg Lys Lys Ser Glu Asn Asp Ile Asp Ser Tyr Lys Ser Ala
 86             195                 200                 205
 88 agg tta gat gaa agt aca tct gaa ggt aca gtg cga aac aaa ggg caa   672
 89 Arg Leu Asp Glu Ser Thr Ser Glu Gly Thr Val Arg Asn Lys Gly Gln
 90         210                 215                 220
 92 ctt gta gac cca cgt ggt tcc aat act agt tca gct gat atc caa cta   720
 93 Leu Val Asp Pro Arg Gly Ser Asn Thr Ser Ser Ala Asp Ile Gln Leu
 94 225                 230                 235                 240
 96 aag ctt aag gag caa agt gac aca ctt tgg aag tta aag gat gga ctt   768
 97 Lys Leu Lys Glu Gln Ser Asp Thr Leu Trp Lys Leu Lys Asp Gly Leu
 98                 245                 250                 255
100 aag act cat gta tcg gct gct gaa tta agg gat atg ctt gag gct aat   816
101 Lys Thr His Val Ser Ala Ala Glu Leu Arg Asp Met Leu Glu Ala Asn
102                 260                 265                 270
104 ggg cag gat aca tca gga cca gaa agg cac cta ttg gat cgc tgt gcg   864
105 Gly Gln Asp Thr Ser Gly Pro Glu Arg His Leu Leu Asp Arg Cys Ala
106             275                 280                 285
108 gat gga atg cta ttt gga gcg ctg ggt cct tgc cca gtc tgt gct aat   912
109 Asp Gly Met Leu Phe Gly Ala Leu Gly Pro Cys Pro Val Cys Ala Asn
110         290                 295                 300
112 ggc atg tac tat tat aat ggt cag tac caa tgc agt ggt aat gtg tca   960
113 Gly Met Tyr Tyr Tyr Asn Gly Gln Tyr Gln Cys Ser Gly Asn Val Ser
114 305                 310                 315                 320
116 gag tgg tcc aag tgt aca tac tct gcc aca gaa cct gtc cgc gtt aag  1008
117 Glu Trp Ser Lys Cys Thr Tyr Ser Ala Thr Glu Pro Val Arg Val Lys
118                 325                 330                 335
120 aag aag tgg caa att cca cat gga aca aag aat gat tac ctt atg aag  1056
121 Lys Lys Trp Gln Ile Pro His Gly Thr Lys Asn Asp Tyr Leu Met Lys
122                 340                 345                 350
124 tgg ttc aaa tct caa aag gtt aag aaa cca gag agg gtt ctt cca cca  1104
125 Trp Phe Lys Ser Gln Lys Val Lys Lys Pro Glu Arg Val Leu Pro Pro
126             355                 360                 365
128 atg tca cct gag aaa tct gga agt aaa gca act cag aga aca tca ttg  1152
129 Met Ser Pro Glu Lys Ser Gly Ser Lys Ala Thr Gln Arg Thr Ser Leu
130         370                 375                 380
132 ctg tct tct aaa ggg ttg gat aaa tta agg ttt tct gtt gta gga caa  1200
133 Leu Ser Ser Lys Gly Leu Asp Lys Leu Arg Phe Ser Val Val Gly Gln
```

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134 385                        390                   395                        400
136 tca aaa gaa gca gca aat gag tgg att gag aag ctc aaa ctt gct ggt   1248
137 Ser Lys Glu Ala Ala Asn Glu Trp Ile Glu Lys Leu Lys Leu Ala Gly
138                    405                   410                   415
140 gcc aac ttc tat gcc agg gtt gtc aaa gat att gat tgt tta att gca   1296
141 Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile Asp Cys Leu Ile Ala
142                420                   425                   430
144 tgt ggt gag ctc gac aat gaa aat gct gaa gtc agg aaa gca agg agg   1344
145 Cys Gly Glu Leu Asp Asn Glu Asn Ala Glu Val Arg Lys Ala Arg Arg
146            435                   440                   445
148 ctg aag ata cca att gta agg gag ggt tac att gga gaa tgt gtt aaa   1392
149 Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile Gly Glu Cys Val Lys
150        450                   455                   460
152 aga aca aaa tgc tgc cat ttg att tgt ata aac tgg aat gcc tta gag   1440
153 Arg Thr Lys Cys Cys His Leu Ile Cys Ile Asn Trp Asn Ala Leu Glu
154 465                    470                   475                   480       1488
156 tcc tca aaa ggc mgt act gtc act gtt aaa gtt aag ggc cga agt gct
W--> 157 Ser Ser Lys Gly Xaa Thr Val Thr Val Lys Val Lys Gly Arg Ser Ala
158                    485  500                  490                   495
160 tgt tca tya agt cct cyg gtt tgc aag aat act gct cac att cct tra   1536
W--> 161 Cys Ser Xaa Ser Pro Xaa Val Cys Lys Asn Thr Ala His Ile Pro Xaa
162                    500                   505                   510
164 gra tgg gaa aag cat ata caa tgc amc ctt aaa cat gtt ctg acc tgn   1584
W--> 164 gra tgg gaa aag cat ata caa tgc amc ctt aaa cat gtt ctg acc tgn
W--> 165 Xaa Trp Glu Lys His Ile Gln Cys Xaa Leu Lys His Val Leu Thr Xaa
166            515                   520                   525
168 cac nag gtg tgy aca ggc tac tat gta ctc cag atc att gaa cag gat   1632
W--> 168 cac nag gtg tgy aca ggc tac tat gta ctc cag atc att gaa cag gat
W--> 169 His Xaa Val Cys Thr Gly Tyr Tyr Val Leu Gln Ile Ile Glu Gln Asp
170        530                   535                   540
172 gat ggg tct gag tgc tac gta ttt cgt aag tgg gga cgg gtt ggg agt   1680
173 Asp Gly Ser Glu Cys Tyr Val Phe Arg Lys Trp Gly Arg Val Gly Ser
174 545                    550                   555                   560
176 gag aaa att gga ggg caa aaa ctg gag gag atg tca aaa act gag gca   1728
177 Glu Lys Ile Gly Gly Gln Lys Leu Glu Glu Met Ser Lys Thr Glu Ala
178                    565                   570                   575
180 atc aag gaa ttc aaa aga tta ttt ctt gag aag act gga aac tca tgg   1776
181 Ile Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr Gly Asn Ser Trp
182                    580                   585                   590
184 gaa gct tgg gaa tgt aaa acc aat ttt cgg aag cag cct ggg aga ttt   1824
185 Glu Ala Trp Glu Cys Lys Thr Asn Phe Arg Lys Gln Pro Gly Arg Phe
186            595                   600                   605
188 tac cca ctt gat gtt gat tat ggt gtt aag aaa gca cca aaa cgg aaa   1872
189 Tyr Pro Leu Asp Val Asp Tyr Gly Val Lys Lys Ala Pro Lys Arg Lys
190        610                   615                   620
192 gat atc agt gaa atg aaa agt tct ctt gct cct caa ttg cta gaa ctc   1920
193 Asp Ile Ser Glu Met Lys Ser Ser Leu Ala Pro Gln Leu Leu Glu Leu
194 625                    630                   635                   640
196 atg aag atg ctt ttc aat gtg gag aca tat aga gct gct atg atg gaa   1968
197 Met Lys Met Leu Phe Asn Val Glu Thr Tyr Arg Ala Ala Met Met Glu
198                    645                   650                   655
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(handwritten annotations in right margin) These Xaas are not listed as individual locations nor as range for sequence listing!

(handwritten) OR. DNA

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         200 ttt gaa awt aat atg tca gaa atg cct ctt ggg aag cta agc mag gra   2016   not listed
W--> 201 Phe Glu Xaa Asn Met Ser Glu Met Pro Leu Gly Lys Leu Ser Xaa Xaa
         202             660             665             670
         204 aat att gag raa gga ttt gaa gca tta act krg rta cmg rat tta ttt   2064
W--> 205 Asn Ile Glu Xaa Gly Phe Glu Ala Leu Thr Xaa Xaa Xaa Xaa Leu Phe
         206         675     2078    680             685                2107
W--> 208 gaa gga cac cgc tna tca agc act ggc ttg ttr gag aaa gct naa ttg   2112
W--> 209 Glu Gly His Arg Xaa Ser Ser Thr Gly Leu Xaa Glu Lys Ala Xaa Leu                    not listed
         210     690             695             700
         212 ttg ytg sga gcm ats syt ttt tca ctc tta tcc ctt cta ttc atc ctc   2160
W--> 213 Leu Xaa Xaa Xaa Xaa Xaa Phe Ser Leu Leu Ser Leu Leu Phe Ile Leu
         214 705             710             715                720
         216 ata tta tac ggg atg agg atg att tca tat tca aag gcg aaa atg ctt   2208
         217 Ile Leu Tyr Gly Met Arg Met Ile Ser Tyr Ser Lys Ala Lys Met Leu
         218             725             730             735
         220 gaa gct ctg cag gat att gaa att gct tca aag ata gtt ggc ttc gat   2256
         221 Glu Ala Leu Gln Asp Ile Glu Ile Ala Ser Lys Ile Val Gly Phe Asp
         222             740             745             750
         224 agc gac agt gat gaa tct ctt gat gat aaa tat atg aaa ctt cac tgt   2304
         225 Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys Leu His Cys
         226             755             760             765
         228 gac atc acc ccg ctg gct cac gat agt gaa gat tac aag tta att gag   2352
         229 Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys Leu Ile Glu
         230     770             775             780
         232 cag tat ctc ctc aac aca cat gct cct act cac aag gac tgg tcg ctg   2400
         233 Gln Tyr Leu Leu Asn Thr His Ala Pro Thr His Lys Asp Trp Ser Leu
         234 785             790             795                800
         236 gaa ctg gag gaa gtt ttt tca ctt gat cga gat gga gaa ctt aat aag   2448
         237 Glu Leu Glu Glu Val Phe Ser Leu Asp Arg Asp Gly Glu Leu Asn Lys
         238             805             810             815
         240 tac tca aga tat aaa aat aat ctg cat aac aag atg cta tta tgg cac   2496
         241 Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu Leu Trp His
         242             820             825             830
         244 ggt tca agg ttg acg aat ttt gtg gga att ctt agt caa ggg cta aga   2544
         245 Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln Gly Leu Arg
         246             835             840             845
         248 att gca cct cct gag gca cct gtt act ggc tat atg ttc ggc aaa ggc   2592
         249 Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly
         250     850             855             860
         252 ctc tac ttt gca gat cta gta agc aag agc gca caa tac tgt tat gtg   2640
         253 Leu Tyr Phe Ala Asp Leu Val Ser Lys Ser Ala Gln Tyr Cys Tyr Val
         254 865             870             875                880
         256 gat agg aat aat cct gta ggt ttg atg ctt ctt tct gag gtt gct tta   2688
         257 Asp Arg Asn Asn Pro Val Gly Leu Met Leu Leu Ser Glu Val Ala Leu
         258             885             890             895
         260 gga gac atg tat gaa cta aag aaa gcc acg tcc atg gac aaa cct cca   2736
         261 Gly Asp Met Tyr Glu Leu Lys Lys Ala Thr Ser Met Asp Lys Pro Pro
         262             900             905             910
         264 aga ggg aag cat tcg acc aag gga tta ggc aaa acc gtg cca ctg gag   2784
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265 Arg Gly Lys His Ser Thr Lys Gly Leu Gly Lys Thr Val Pro Leu Glu
266           915                 920                 925
268 tca gag ttt gtg aag tgg agg gat gat gtc gta gtt ccc tgc ggc aag    2832
269 Ser Glu Phe Val Lys Trp Arg Asp Asp Val Val Val Pro Cys Gly Lys
270           930                 935                 940
272 ccg gtg cca tca tca att agg agc tct gaa ctc atg tac aat gag tac    2880
273 Pro Val Pro Ser Ser Ile Arg Ser Ser Glu Leu Met Tyr Asn Glu Tyr
274 945                 950                 955                 960
276 atc gtc tac aac aca tcc cag gtg aag atg cag ttc ttg ctg aag gtg    2928
277 Ile Val Tyr Asn Thr Ser Gln Val Lys Met Gln Phe Leu Leu Lys Val
278                 965                 970                 975
                                                                       2949
280 cgt ttc cat cac aag agg tag
281 Arg Phe His His Lys Arg  *
282           980
285 <210> SEQ ID NO: 2
286 <211> LENGTH: 982
287 <212> TYPE: PRT
288 <213> ORGANISM: Zea mays
290 <220> FEATURE:
291 <221> NAME/KEY: VARIANT
292 <222> LOCATION: 485, 499, 502, 512, 513, 521, 528, 530, 659, 671, 672, 676,
293          683, 684, 685, 686, 693, 699, 703, 706, 707, 708, 709, 710
294 <223> OTHER INFORMATION: Xaa = Any Amino Acid
296 <400> SEQUENCE: 2
297 Met Ala Ala Pro Pro Lys Ala Trp Lys Ala Glu Tyr Ala Lys Ser Gly
298 1                 5                 10                 15
299 Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Gln Leu
300           20                 25                 30
301 Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro
302           35                 40                 45
303 Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys
304       50                 55                 60
305 Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln
306 65                 70                 75                 80
307 Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly Thr Ser Ser
308                 85                 90                 95
309 Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala
310           100                 105                 110
311 Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys Gly Ser Val
312           115                 120                 125
313 Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly Ile Pro Trp
314       130                 135                 140
315 Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu
316 145                 150                 155                 160
317 Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met
318                 165                 170                 175
319 Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn Glu Gln Asn Lys Gly
320           180                 185                 190
321 Ser Lys Arg Lys Lys Ser Glu Asn Asp Ile Asp Ser Tyr Lys Ser Ala
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/236,995D

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Input Set : **A:\Seqlist.txt**
Output Set: **N:\CRF3\10292001\I236995D.raw**

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L:157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:213 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:359 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:381 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:383 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
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